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Claims 1-16 (Canceled).

17. (Previously Amended) The method of claim 39, wherein the primers consist of 25 to 40 nucleotides.

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18. (Previously Amended) The method of claim 39, further comprising, labeling said PCR products, denaturing said labeled PCR products, and contacting the denatured labeled PCR products with a nucleotide sequence complementary to a fusion partner nucleotide sequence.

19. (Previously Added) The method of claim 18, wherein said complementary nucleotide sequence is a nucleotide probe covalently bonded on a support.

20. (Previously Added) The method of claim 18, wherein said probes are labeled and are present in solution.

21. (Previously Amended) The method of claim 39, wherein one of the primers consists of a sequence containing a cassette of 40 to 60 nucleotides and 10 to 20 T nucleotides, and the second primer is a random repeat of nucleotides.

Claims 22-23 (Canceled).

24. (Currently Amended) The method of ~~claim 22~~claim 39, wherein the rearrangements of the target gene is a translocation associated with the MLL gene.

25. (Currently Amended) The method of claim 24, comprising

a) the RT synthesis of a cDNA pool from the patient's RNA, using primers ~~with a cassette and a known nucleotide sequence~~,

b) a PCR amplification using a first primer located on the MLL exon 5, as specific sense primer, the 3' primer being complementary to the ~~oligonucleotide cassette~~ known nucleotide sequence used in the RT step.

26. (Currently Amended) The method of ~~claim 24~~ claim 25, further comprising a further PCR amplification, as a nested amplification cycle after step (b) ~~second nested amplification cycle~~, using an internal sense primer with respect to the first MLL-primer, where the 3' primer is the same on each cycle and complementary to the ~~oligonucleotide cassette~~ known nucleotide sequence used in the RT step.

27. (Currently Amended) The method of claim 24, further comprising, for detecting fusion transcripts,

e) contacting ~~a) contacting~~ a probe specific for known MLL fusion partners, with denatured PCR products of step (b) wherein said PCR products have been denatured and labeled with digoxigenine, in order to hybridize said probe with the PCR products where complementary bases are present, and providing hybridization products

f) contacting ~~b) contacting~~ the hybridization products, when obtained, with anti-digoxigenine antibodies coupled to with an enzyme and capable of reacting with a substrate of said ~~to react with the enzyme substrate to release by releasing~~ a detectable product, said contacting thereby producing a probe/PCR product reactive complex and

g) contacting ~~e) contacting~~ the probe/PCR product reactive complex ~~mixture~~ with the ~~enzyme~~-substrate, and

h) detecting ~~d) detecting~~ the detectable product so formed, if any.

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cont.  
Claim 28 (Canceled).

29. (Previously Amended) The method of claim 39, wherein said cancer is leukemia.

30. (Previously Amended) The method of claim 39, wherein said cancer is a solid tumor.

31. (Previously Amended) The method of claim 30, wherein said cancer is a Ewing tumor.

32. (Currently Amended) A kit for identifying DNA sequences of fusion genes, said fusion genes comprising a target gene and a fusion partner, said kit comprising: one pair of primers wherein one of the primers of the pair is complementary to the nucleotide sequence of the target gene and binds to said target gene to form a complex

which provides indiscriminate amplification, ~~in the presence of Taq polymerase, and~~ and  
the other primer is an anchored primer; and at least one probe specific for said fusion  
partner, said at least one probe being bound to a solid support.

Claims 33-35 (Canceled).

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cont.  
36. (Previously Amended) A kit according to claim 32, wherein said at least one  
probe is bound to the solid support through a biotin group bonded to streptavidine  
coupled to said support.

37. (Previously Amended) A kit according to claim 32, wherein the solid support  
is a miniaturized support.

38. (Previously Amended) A kit according to claim 32 wherein the support is a  
DNA chip.

39. (Previously Amended) An *in vitro* diagnostic method for detecting and  
identifying DNA sequences of fusion genes comprising a target gene and a fusion  
partner, said fusion genes being involved in cancer associated with rearrangements of  
the target gene, wherein a patient DNA or cDNA is subjected to an anchored PCR  
comprising:

a) indiscriminately amplifying all of the DNA or cDNA of said fusion genes by  
PCR, with one pair of primers, one of the primers being complementary to the

nucleotide sequence of the target gene, the other primer being an anchored primer, wherein all the DNA or cDNA sequences of the target gene are amplified,

- b) obtaining PCR products,
- c) hybridizing the PCR products with probes specific for said fusion partner,
- d) detecting rearrangements of the target gene, and identifying the fusion genes of any detected rearrangements.

40. (new) The method of claim 24, comprising, for detecting fusion transcripts,

a) contacting a probe specific for known MLL fusion partners, with denatured labeled PCR products, in order to hybridize said probe with the PCR products where complementary bases are present,

b) contacting the hybridization products, when obtained, with marked antibodies directed against said labeled PCR products, said marked antibodies being coupled to an enzyme and being capable of reacting with the enzyme substrate by releasing a detectable product, and

c) contacting the probe/PCR product reactive mixture with the enzyme substrate, and

d) detecting the product so formed, if any.

41. (new) The method of claim 40, wherein said denatured labeled PCR products are labeled with biotin or a fluorophore.

42. (new) The kit of claim 32 wherein said target gene is the MLL gene.